

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/785,452A
Source: IFWO
Date Processed by STIC: 10/29/04

ENTERED



IFWO

RAW SEQUENCE LISTING

DATE: 10/29/2004

PATENT APPLICATION: US/10/785,452A

TIME: 12:55:44

Input Set : N:\LMOORE\pto.lm.txt

Output Set: N:\CRF4\10292004\J785452A.raw

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4 <110> APPLICANT: Tillett, D
5   Thomas, T
7 <120> TITLE OF INVENTION: A method of sequestering and/or purifying a polypeptide
9 <130> FILE REFERENCE: nuc2004
11 <140> CURRENT APPLICATION NUMBER: 10/785,452A
13 <141> CURRENT FILING DATE: 2004-02-25
15 <150> PRIOR APPLICATION NUMBER: PCT/AU02/01159
17 <151> PRIOR FILING DATE: 2002-08-27
19 <160> NUMBER OF SEQ ID NOS: 12
21 <210> SEQ ID NO: 1
23 <211> LENGTH: 714
25 <212> TYPE: DNA
27 <213> ORGANISM: Aequorea victoria
29 <400> SEQUENCE: 1
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31 Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
32 1 5 10 15
34 gtt gaa tta gat ggc gat gtt aat ggg caa aaa ttc tct gtc agt 90
35 Val Glu Leu Asp Gly Asp Val Asn Gly Gln Lys Phe Ser Val Ser
36 20 25 30
38 gga gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctt aaa 135
39 Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys
40 35 40 45
42 ttt att tgc act act ggg aag cta cct gtt cca tgg cca aca ctt 180
43 Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu
44 50 55 60
46 gtc act act ttc gcg tat ggt ctt caa tgc ttt gcg aga tac cca 225
47 Val Thr Thr Phe Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro
48 65 70 75
50 gat cat atg aaa cag cat gac ttt ttc aag agt gcc atg ccc gaa 270
51 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu
52 80 85 90
54 ggt tat gta cag gaa aga act ata ttt tac aaa gat gac ggg aac 315
55 Gly Tyr Val Gln Glu Arg Thr Ile Phe Tyr Lys Asp Asp Gly Asn
56 95 100 105
58 tac aag aca cgt gct gaa gtc aag ttt gaa ggt gat acc ctt gtt 360
59 Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val
60 110 115 120
62 aat aga atc gag tta aaa ggt att gat ttt aaa gaa gat gga aac 405
63 Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
64 125 130 135
66 att ctt gga cac aaa atg gaa tac aac tat aac tca cat aat gta 450
67 Ile Leu Gly His Lys Met Glu Tyr Asn Tyr Asn Ser His Asn Val

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68          140          145          150
70 tac atc atg gca gac aaa cca aag aat gga atc aaa gtt aac ttc 495
71 Tyr Ile Met Ala Asp Lys Pro Lys Asn Gly Ile Lys Val Asn Phe
72          155          160          165
74 aaa att aga cac aac att aaa gat gga agc gtt caa tta gca gac 540
75 Lys Ile Arg His Asn Ile Lys Asp Gly Ser Val Gln Leu Ala Asp
76          170          175          180
78 cat tat caa caa aat act cca att ggc gat ggc cct gtc ctt tta 585
79 His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
80          185          190          195
82 cca gac aac cat tac ctg tcc aca caa tct gcc ctt tcc aaa gat 630
83 Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp
84          200          205          210
86 ccc aac gaa aag aga gat cac atg atc ctt ctt gag ttt gta aca 675
87 Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu Glu Phe Val Thr
88          215          220          225
90 gct gct ggg att aca cat ggc atg gat gaa cta tac aaa 714
91 Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
92          230          235          238
96 <210> SEQ ID NO: 2
98 <211> LENGTH: 1149
100 <212> TYPE: DNA
102 <213> ORGANISM: Escherichia coli
104 <400> SEQUENCE: 2
105 atg ttt gaa cca atg gaa ctt acc aat gac gcg gtg att aaa gtc 45
106 Met Phe Glu Pro Met Glu Leu Thr Asn Asp Ala Val Ile Lys Val
107 1          5          10          15
109 atc ggc gtc ggc ggc ggc ggc ggt aat gct gtt gaa cac atg gtg 90
110 Ile Gly Val Gly Gly Gly Gly Gly Asn Ala Val Glu His Met Val
111          20          25          30
113 cgc gag cgc att gaa ggt gtt gaa ttc ttc gcg gta aat acc gat 135
114 Arg Glu Arg Ile Glu Gly Val Glu Phe Phe Ala Val Asn Thr Asp
115          35          40          45
117 gca caa gcg ctg cgt aaa aca gcg gtt gga cag acg att caa atc 180
118 Ala Gln Ala Leu Arg Lys Thr Ala Val Gly Gln Thr Ile Gln Ile
119          50          55          60
121 ggt agc ggt atc acc aaa gga ctg ggc gct ggc gct aat cca gaa 225
122 Gly Ser Gly Ile Thr Lys Gly Leu Gly Ala Gly Ala Asn Pro Glu
123          65          70          75
125 gtt ggc cgc aat gcg gct gat gag gat cgc gat gca ttg cgt gcg 270
126 Val Gly Arg Asn Ala Ala Asp Glu Asp Arg Asp Ala Leu Arg Ala
127          80          85          90
129 gcg ctg gaa ggt gca gac atg gtc ttt att gct gcg ggt atg ggt 315
130 Ala Leu Glu Gly Ala Asp Met Val Phe Ile Ala Ala Gly Met Gly
131          95          100          105
133 ggt ggt acc ggt aca ggt gcg gca cca gtc gtc gct gaa gtg gca 360
134 Gly Gly Thr Gly Thr Gly Ala Ala Pro Val Val Ala Glu Val Ala
135          110          115          120
137 aaa gat ttg ggt atc ctg acc gtt gct gtc gtc act aag cct ttc 405

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138 Lys Asp Leu Gly Ile Leu Thr Val Ala Val Val Thr Lys Pro Phe
139          125          130          135
141 aac ttt gaa ggc aag aag cgt atg gca ttc gcg gag cag ggg atc 450
142 Asn Phe Glu Gly Lys Lys Arg Met Ala Phe Ala Glu Gln Gly Ile
143          140          145          150
145 act gaa ctg tcc aag cat gtg aac tct ctg atc act atc ccg aac 495
146 Thr Glu Leu Ser Lys His Val Asn Ser Leu Ile Thr Ile Pro Asn
147          155          160          165
149 gac aaa ctg ctg aaa gtt ctg ggc cgc ggt atc tcc ctg ctg gat 540
150 Asp Lys Leu Leu Lys Val Leu Gly Arg Gly Ile Ser Leu Leu Asp
151          170          175          180
153 gcg ttt ggc gca gcg aac gat gta ctg aaa ggc gct gtg caa ggt 585
154 Ala Phe Gly Ala Ala Asn Asp Val Leu Lys Gly Ala Val Gln Gly
155          185          190          195
157 atc gct gaa ctg att act cgt ccg ggt ttg atg aac gtg gac ttt 630
158 Ile Ala Glu Leu Ile Thr Arg Pro Gly Leu Met Asn Val Asp Phe
159          200          205          210
161 gca gac gta cgc acc gta atg tct gag atg ggc cac gca atg atg 675
162 Ala Asp Val Arg Thr Val Met Ser Glu Met Gly His Ala Met Met
163          215          220          225
165 ggt tct ggc gtg gcg agc ggt gaa gac cgt gcg gaa gaa gct gct 720
166 Gly Ser Gly Val Ala Ser Gly Glu Asp Arg Ala Glu Glu Ala Ala
167          230          235          240
169 gaa atg gct atc tct tct ccg ctg ctg gaa gat atc gac ctg tct 765
170 Glu Met Ala Ile Ser Ser Pro Leu Leu Glu Asp Ile Asp Leu Ser
171          245          250          255
173 ggc gcg cgc ggc gtg ctg gtt aac atc acg gcg ggc ttc gac ctg 810
174 Gly Ala Arg Gly Val Leu Val Asn Ile Thr Ala Gly Phe Asp Leu
175          260          265          270
177 cgt ctg gat gag ttc gaa acg gta ggt aac acc atc cgt gca ttt 855
178 Arg Leu Asp Glu Phe Glu Thr Val Gly Asn Thr Ile Arg Ala Phe
179          275          280          285
181 gct tcc gac aac gcg act gtg gtt atc ggt act tct ctt gac ccg 900
182 Ala Ser Asp Asn Ala Thr Val Val Ile Gly Thr Ser Leu Asp Pro
183          290          295          300
185 gat atg aat gac gag ctg cgc gta acc gtt gtt gcg aca ggt atc 945
186 Asp Met Asn Asp Glu Leu Arg Val Thr Val Val Ala Thr Gly Ile
187          305          310          315
189 ggc atg gac aaa cgt cct gaa atc act ctg gtg acc aat aag cag 990
190 Gly Met Asp Lys Arg Pro Glu Ile Thr Leu Val Thr Asn Lys Gln
191          320          325          330
193 gtt cag cag cca gtg atg gat cgc tac cag cag cat ggg atg gct 1035
194 Val Gln Gln Pro Val Met Asp Arg Tyr Gln Gln His Gly Met Ala
195          335          340          345
197 ccg ctg acc caa gag cag aag ccg gtt gct aaa gtc gtg aat gac 1080
198 Pro Leu Thr Gln Glu Gln Lys Pro Val Ala Lys Val Val Asn Asp
199          350          355          360
201 aat gcg ccg caa act gcg aaa gag ccg gat tat ctg gat atc cca 1125
202 Asn Ala Pro Gln Thr Ala Lys Glu Pro Asp Tyr Leu Asp Ile Pro

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203          365          370          375
205 gca ttc ctg cgt aag caa gct gat 1149
206 Ala Phe Leu Arg Lys Gln Ala Asp
207          380          383
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213 <211> LENGTH: 546
215 <212> TYPE: DNA
217 <213> ORGANISM: Human rhinovirus
219 <400> SEQUENCE: 3
220 gga cca aac aca gaa ttt gca cta tcc ctg tta agg aaa aac ata 45
221 Gly Pro Asn Thr Glu Phe Ala Leu Ser Leu Leu Arg Lys Asn Ile
222 1          5          10          15
224 atg act ata aca acc tca aag gga gag ttc aca ggg tta ggc ata 90
225 Met Thr Ile Thr Thr Ser Lys Gly Glu Phe Thr Gly Leu Gly Ile
226          20          25          30
228 cat gat cgt gtc tgt gtg ata ccc aca cac gca cag cct ggt gat 135
229 His Asp Arg Val Cys Val Ile Pro Thr His Ala Gln Pro Gly Asp
230          35          40          45
232 gat gta cta gtg aat ggt cag aaa att aga gtt aag gat aag tac 180
233 Asp Val Leu Val Asn Gly Gln Lys Ile Arg Val Lys Asp Lys Tyr
234          50          55          60
236 aaa tta gta gat cca gag aac att aat cta gag ctt aca gtg ttg 225
237 Lys Leu Val Asp Pro Glu Asn Ile Asn Leu Glu Leu Thr Val Leu
238          65          70          75
240 act tta gat aga aat gaa aaa ttc aga gat atc agg gga ttt ata 270
241 Thr Leu Asp Arg Asn Glu Lys Phe Arg Asp Ile Arg Gly Phe Ile
242          80          85          90
244 tca gaa gat cta gaa ggt gtg gat gcc act ttg gta gta cat tca 315
245 Ser Glu Asp Leu Glu Gly Val Asp Ala Thr Leu Val Val His Ser
246          95          100          105
248 aat aac ttt acc aac act atc tta gaa gtt ggc cct gta aca atg 360
249 Asn Asn Phe Thr Asn Thr Ile Leu Glu Val Gly Pro Val Thr Met
250          110          115          120
252 gca gga ctt att aat ttg agt agc acc ccc act aac aga atg att 405
253 Ala Gly Leu Ile Asn Leu Ser Ser Thr Pro Thr Asn Arg Met Ile
254          125          130          135
258 cgt tat gat tat gca aca aaa act ggg cag tgt gga ggt gtg ctg 450
259 Arg Tyr Asp Tyr Ala Thr Lys Thr Gly Gln Cys Gly Gly Val Leu
260          140          145          150
262 tgt gct act ggt aag atc ttt ggt att cat gtt ggc ggt aat gga 495
263 Cys Ala Thr Gly Lys Ile Phe Gly Ile His Val Gly Gly Asn Gly
264          155          160          165
266 aga caa gga ttt tca gct caa ctt aaa aaa caa tat ttt gta gag 540
267 Arg Gln Gly Phe Ser Ala Gln Leu Lys Lys Gln Tyr Phe Val Glu
268          170          175          180
270 aaa caa 546
271 Lys Gln
272          182
276 <210> SEQ ID NO: 4

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278 <211> LENGTH: 27
 280 <212> TYPE: DNA
 282 <213> ORGANISM: artificial sequence
 284 <220> FEATURE:
 286 <223> OTHER INFORMATION: Polymerase chain reaction oligonucleotide primer
 288 <400> SEQUENCE: 4
 290 atcatgagta aaggagaaga actttttc 27
 294 <210> SEQ ID NO: 5
 296 <211> LENGTH: 29
 298 <212> TYPE: DNA
 300 <213> ORGANISM: artificial sequence
 302 <220> FEATURE:
 304 <223> OTHER INFORMATION: Polymerase chain reaction oligonucleotide primer
 306 <400> SEQUENCE: 5
 307 aggatcctta tttgtatagt tcatccatg 29
 311 <210> SEQ ID NO: 6
 313 <211> LENGTH: 24
 315 <212> TYPE: DNA
 317 <213> ORGANISM: artificial sequence
 319 <220> FEATURE:
 321 <223> OTHER INFORMATION: OTHER INFORMATION: Polymerase chain reaction oligonucleotide
 primer
 323 <400> SEQUENCE: 6
 324 ggcataatggt tgaaccaatg gaac 24
 328 <210> SEQ ID NO: 7
 330 <211> LENGTH: 27
 332 <212> TYPE: DNA
 334 <213> ORGANISM: artificial sequence
 336 <220> FEATURE:
 338 <223> OTHER INFORMATION: Polymerase chain reaction oligonucleotide primer
 340 <400> SEQUENCE: 7
 341 gtccatgggc ccttgaaata gtacttc 27
 345 <210> SEQ ID NO: 8
 347 <211> LENGTH: 43
 349 <212> TYPE: DNA
 351 <213> ORGANISM: artificial sequence
 353 <220> FEATURE:
 355 <223> OTHER INFORMATION: Polymerase chain reaction oligonucleotide primer
 357 <400> SEQUENCE: 8
 358 gggcccttga aatagtactt ctagatcagc ttgcttacgc agg 43
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 364 <211> LENGTH: 27
 366 <212> TYPE: DNA
 368 <213> ORGANISM: artificial sequence
 370 <220> FEATURE:
 372 <223> OTHER INFORMATION: Polymerase chain reaction oligonucleotide primer
 374 <400> SEQUENCE: 9
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 379 <210> SEQ ID NO: 10
 381 <211> LENGTH: 32

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/785,452A

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Input Set : N:\LMOORE\pto.lm.txt

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